

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 16:48:48 / Search time 1490.17 Seconds
Sequence: 1217.774 Million cell updates/sec

Title: US-09-486-094-1

Perfect score: 1 agctccgtgcagcagat.....gaagcgtgcagcagatcgcg 110

Scoring table: IDENTITY_NUC

Gapop 10.0, capext 1.0

Searched: 1672140 seqs, 8246589755 residues

Total number of hits satisfying chosen parameters: 254280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Maximum Match 10%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: gb-ph.*

2: gb-ph.*

3: gb-ph.*

4: gb-ph.*

5: gb-ph.*

6: gb-ph.*

7: gb-ph.*

8: gb-ph.*

9: gb-ph.*

10: gb-ph.*

11: gb-ph.*

12: gb-ph.*

13: gb-ph.*

14: gb-ph.*

15: gb-ph.*

16: gb-ph.*

17: gb-ph.*

18: gb-ph.*

19: gb-ph.*

20: gb-ph.*

21: gb-ph.*

22: gb-ph.*

23: gb-ph.*

24: gb-ph.*

25: gb-ph.*

26: gb-ph.*

27: gb-ph.*

28: gb-ph.*

29: gb-ph.*

30: gb-ph.*

31: gb-ph.*

32: gb-ph.*

33: gb-ph.*

34: gb-ph.*

35: gb-ph.*

36: gb-ph.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	110	100.0	110	6	A58893	A58893 Sequence 1
2	110	100.0	211	6	A58895	A58895 Sequence 3
3	44	40.0	44	6	A58896	A58896 Sequence 6
4	44	40.0	44	6	A58898	A58898 Sequence 9
5	35	31.8	87	6	A5931	A5931 Sequence 6
6	34	30.9	109	6	A5931	A5931 Sequence 3
7	34	30.9	109	6	A5931	A5931 Sequence 9
8	34	30.9	169	6	A5931	A5931 Sequence 3
9	34	30.9	169	6	A5931	A5931 Sequence 9
10	31.6	28.7	1430	14	A5931	A5931 Sequence 3
11	31.6	28.7	1430	14	A5931	A5931 Sequence 9
12	31.6	28.7	1430	14	A5931	A5931 Sequence 3
13	31.6	28.7	1430	14	A5931	A5931 Sequence 9
14	30.2	27.5	14875	2	A5931	A5931 Sequence 3
15	30.2	27.5	14875	2	A5931	A5931 Sequence 9
16	30.2	27.5	14875	2	A5931	A5931 Sequence 3
17	30.2	27.5	14875	2	A5931	A5931 Sequence 9
18	30.2	27.5	14875	2	A5931	A5931 Sequence 3
19	30.2	27.5	14875	2	A5931	A5931 Sequence 9
20	30.2	27.5	14875	2	A5931	A5931 Sequence 3
21	29.8	27.1	11957	2	A5931	A5931 Sequence 9
22	29.8	27.1	11957	2	A5931	A5931 Sequence 3
23	29.8	27.1	11957	2	A5931	A5931 Sequence 9
24	29.8	27.1	11957	2	A5931	A5931 Sequence 3
25	29.8	27.1	11957	2	A5931	A5931 Sequence 9
26	29.8	27.1	11957	2	A5931	A5931 Sequence 3
27	29.8	27.1	11957	2	A5931	A5931 Sequence 9
28	29.8	27.1	11957	2	A5931	A5931 Sequence 3
29	29.8	27.1	11957	2	A5931	A5931 Sequence 9
30	29.8	27.1	11957	2	A5931	A5931 Sequence 3
31	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
32	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
33	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
34	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
35	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
36	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
37	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
38	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
39	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
40	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
41	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
42	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
43	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
44	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S
45	28.6	26.0	37134	11	G43892	G43892 WAF-3511-S

ALIGNMENTS

RESULT	1
LOCUS	A58893
DEFINITION	Sequence 1 from Patent DNA9099189.
VERSION	A58893.1 GI:6781852
KEYWORDS	unclassified.
ORGANISM	unclassified.
REFERENCE	unclassified.
TITLE	GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED FROM THE SAME VECTOR
JOURNAL	DEBROE RICHARD (FR); JOFFMAN JULES (FR)
FEATURES	Location/Qualifiers
source	/organism="unidentified"
	/db_xref="taxon:32544"

25-JAN-2000


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Query Match          27.5%; Score 30.2; DB 2; Length 148975;
Best Local Similarity 69.5%; Pred. NO. 15;
Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Cy 1 aggtcgtgctggcagatcagatcgcagagagggggtgtgtactacaagt 59
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116802 AGGACGATGAGCTTGGAGACGATGAGCTACAGAGGAGGGTGGTTTCATAAATCTG 116860

RESULT 15
AR036572/C      AR036572  246240 bp      DNN      29-SEP-1999
LOCUS          AR036572  20 From Patent US 5872237.
ACCESSION      AR036572
VERSION        AR036572.1 GI:5953240
DEFINITION     Bacteriophage phi21 genome.
KEYWORDS       Bacteriophage; DNA; Genomic; Sequence;
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      Unpublished.
AUTHORS        Feder, J. Nathan, Krommal, G. Scott, Lauer, P. M., Ruddy, D. A., Thomas, W.,
                Tsuchihashi, Z., and Wolff, R. K.
TITLE          Bacteriophage phi21 genome.
JOURNAL        Patent: US 5872237-A 20 16-FEB-1999;
FEATURES       Location/Qualifiers
                .. source          phi21
                .. organism       /organism="unknown"
BASE COUNT     73211 a 50177 c 50599 g 72252 t      1 others
ORIGIN

Query Match          27.5%; Score 30.2; DB 6; Length 246240;
Best Local Similarity 69.5%; Pred. NO. 15;
Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Cy 1 aggtcgtgctggcagatcagatcgcagagagggggtgtgtactacaagt 59
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47382 AGGACGATGAGCTTGGAGACGATGAGCTACAGAGGAGGGTGGTTTCATAAATCTG 47324

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Search completed: April 1 2, 2002, 21:29:29
 Job time: 9641 sec